# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 16:21:00*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524683.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524683 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524683.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 16:20:58 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524683.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,925,097 |
| Mapped reads | 1,773,504 / 92.13% |
| Unmapped reads | 151,593 / 7.87% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,655 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 77,541 / 4.03% |
| Duplication rate | 3.25% |
| Clipped reads | 1,776,715 / 92.29% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 27,073,433 / 25.96% |
| Number/percentage of C's | 19,401,299 / 18.61% |
| Number/percentage of T's | 33,539,418 / 32.16% |
| Number/percentage of G's | 24,250,238 / 23.26% |
| Number/percentage of N's | 14,113 / 0.01% |
| GC Percentage | 41.86% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0337 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3108 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.69 |

## 2.5. Mismatches and indels

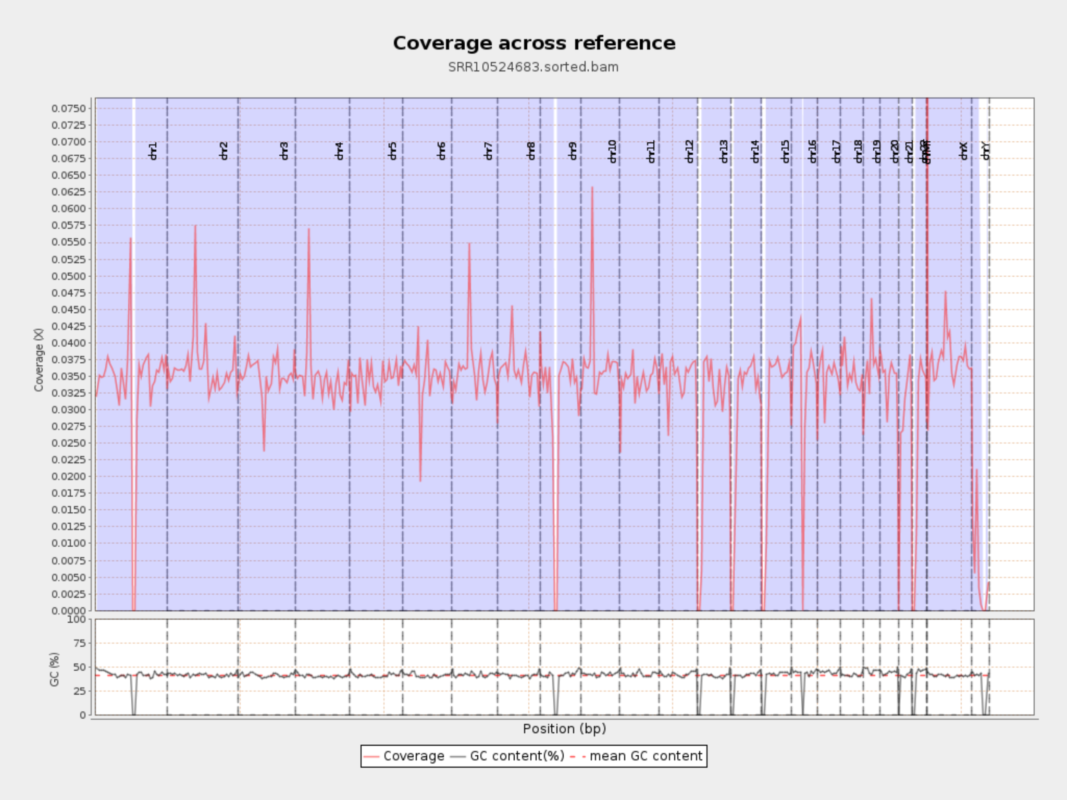
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 521,446 |
| Insertions | 7,897 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 19,763 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 42.91% |

## 2.6. Chromosome stats

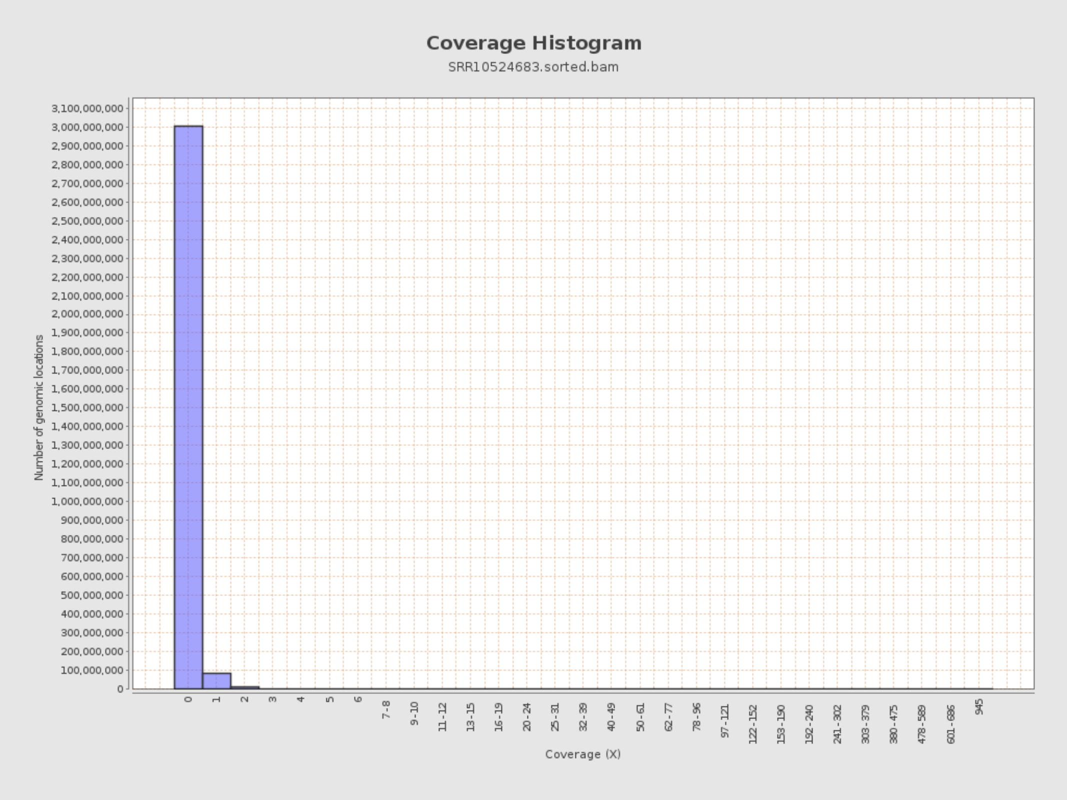
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8356706 | 0.0335 | 0.5218 |
| chr2 | 243199373 | 8878476 | 0.0365 | 0.4558 |
| chr3 | 198022430 | 6927041 | 0.035 | 0.2061 |
| chr4 | 191154276 | 6712132 | 0.0351 | 0.2392 |
| chr5 | 180915260 | 6287572 | 0.0348 | 0.207 |
| chr6 | 171115067 | 6013433 | 0.0351 | 0.2408 |
| chr7 | 159138663 | 5781594 | 0.0363 | 0.3685 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5280404 | 0.0361 | 0.3549 |
| chr9 | 141213431 | 4355896 | 0.0308 | 0.2543 |
| chr10 | 135534747 | 5058547 | 0.0373 | 0.3132 |
| chr11 | 135006516 | 4659525 | 0.0345 | 0.2663 |
| chr12 | 133851895 | 4698685 | 0.0351 | 0.209 |
| chr13 | 115169878 | 3304044 | 0.0287 | 0.1866 |
| chr14 | 107349540 | 3118364 | 0.029 | 0.1945 |
| chr15 | 102531392 | 2996083 | 0.0292 | 0.1917 |
| chr16 | 90354753 | 3036828 | 0.0336 | 0.2203 |
| chr17 | 81195210 | 2864529 | 0.0353 | 0.2214 |
| chr18 | 78077248 | 2774098 | 0.0355 | 0.4779 |
| chr19 | 59128983 | 2171276 | 0.0367 | 0.4055 |
| chr20 | 63025520 | 2181044 | 0.0346 | 0.2091 |
| chr21 | 48129895 | 1381854 | 0.0287 | 0.2167 |
| chr22 | 51304566 | 1249042 | 0.0243 | 0.1726 |
| chrMT | 16571 | 64746 | 3.9072 | 2.7738 |
| chrX | 155270560 | 5816378 | 0.0375 | 0.2354 |
| chrY | 59373566 | 341441 | 0.0058 | 0.1982 |

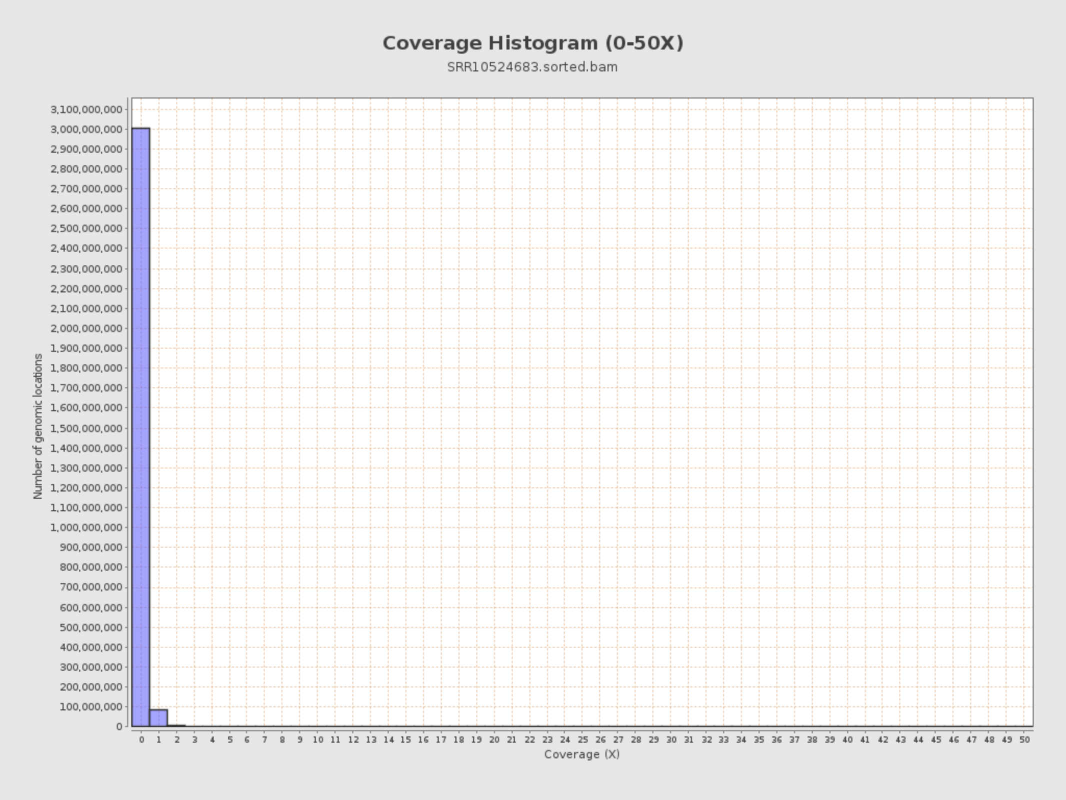
# 3. Results : Coverage across reference



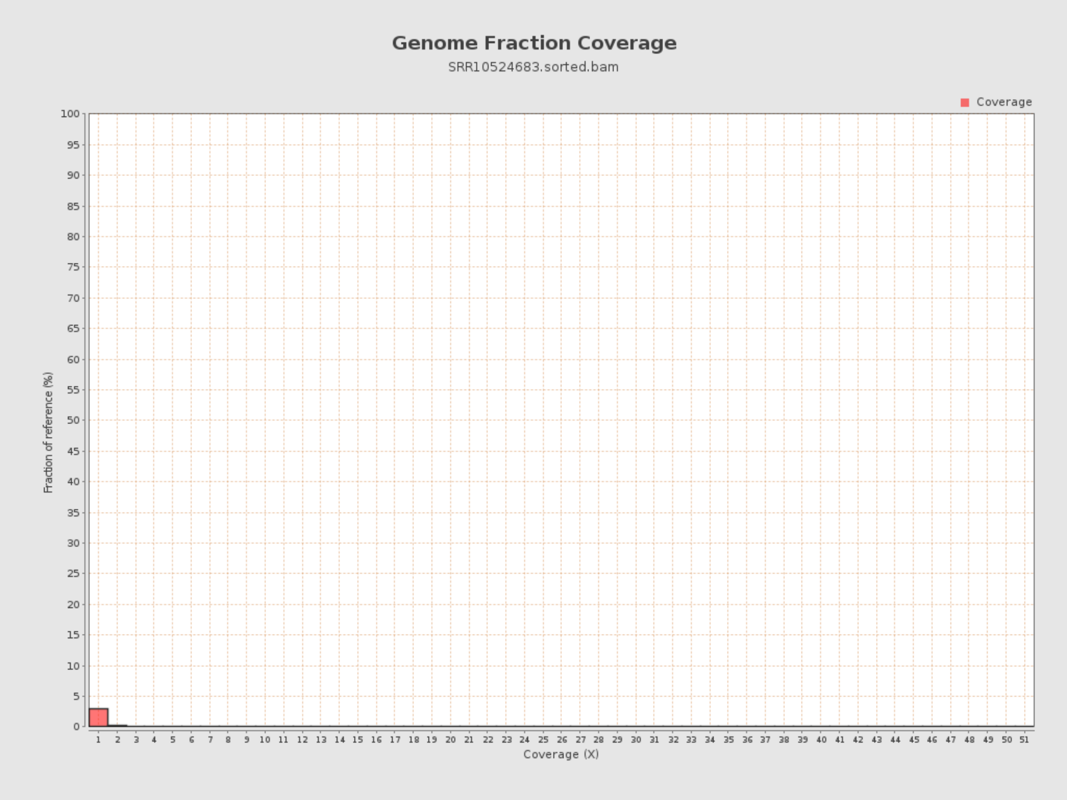
# 4. Results : Coverage Histogram



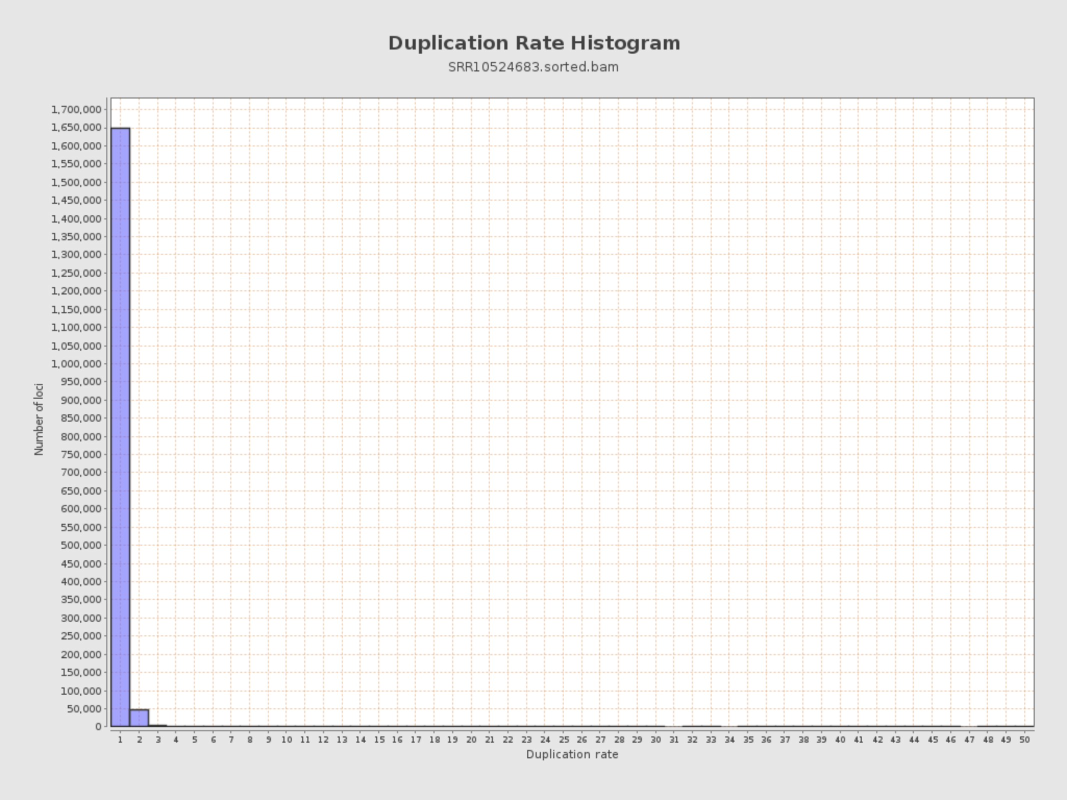
# 5. Results : Coverage Histogram (0-50X)



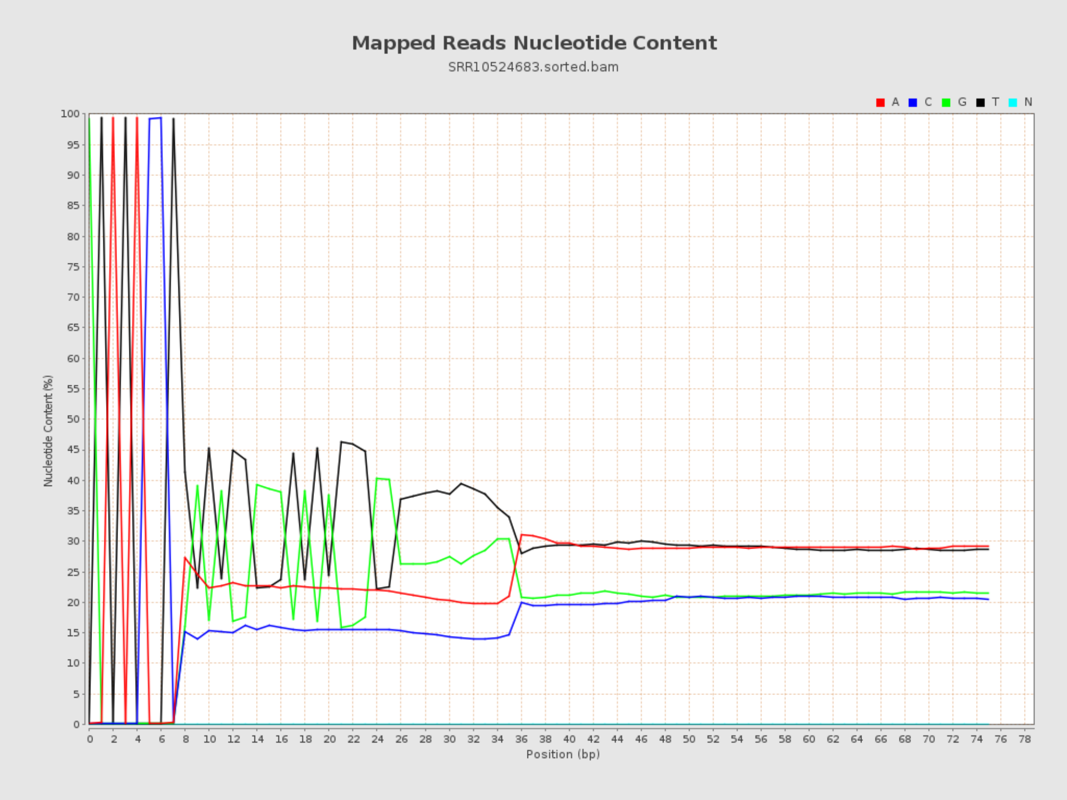
# 6. Results : Genome Fraction Coverage



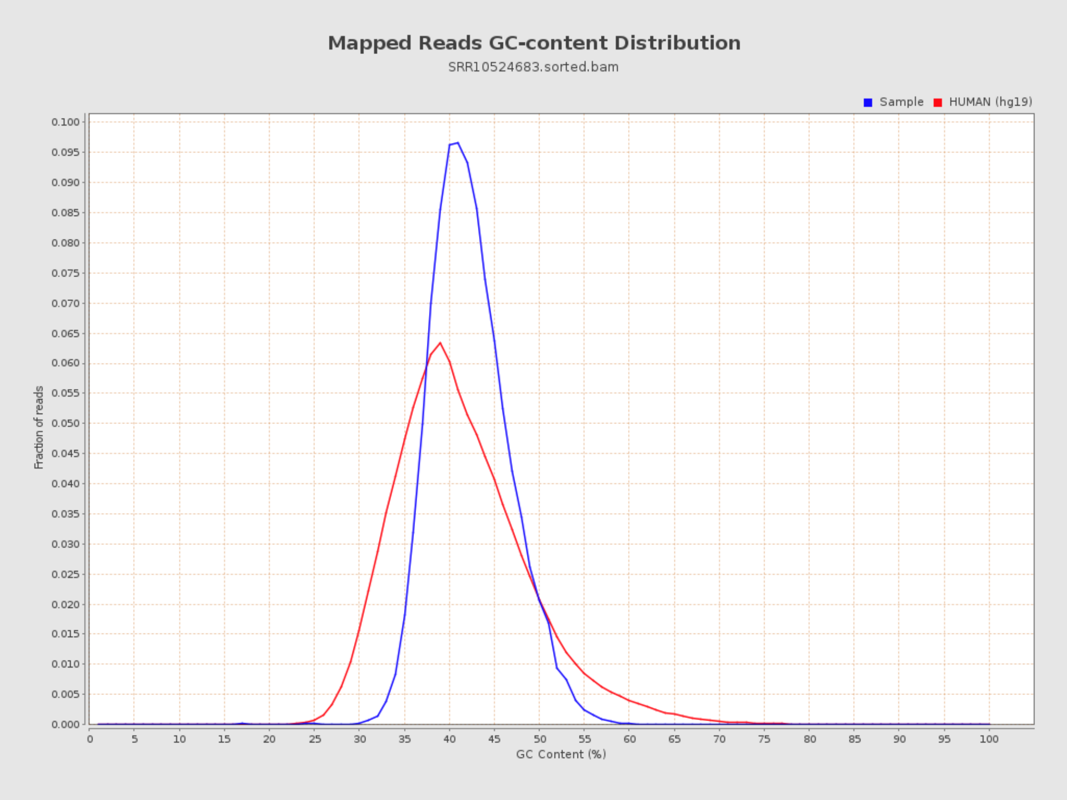
# 7. Results : Duplication Rate Histogram



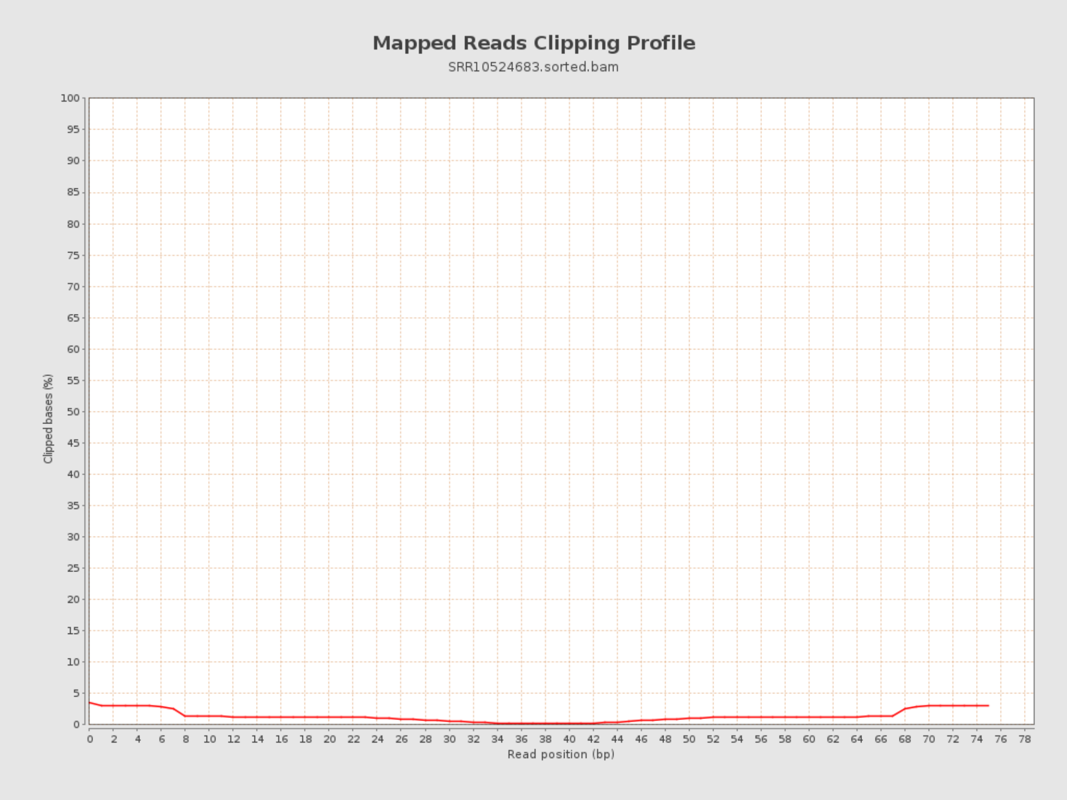
# 8. Results : Mapped Reads Nucleotide Content



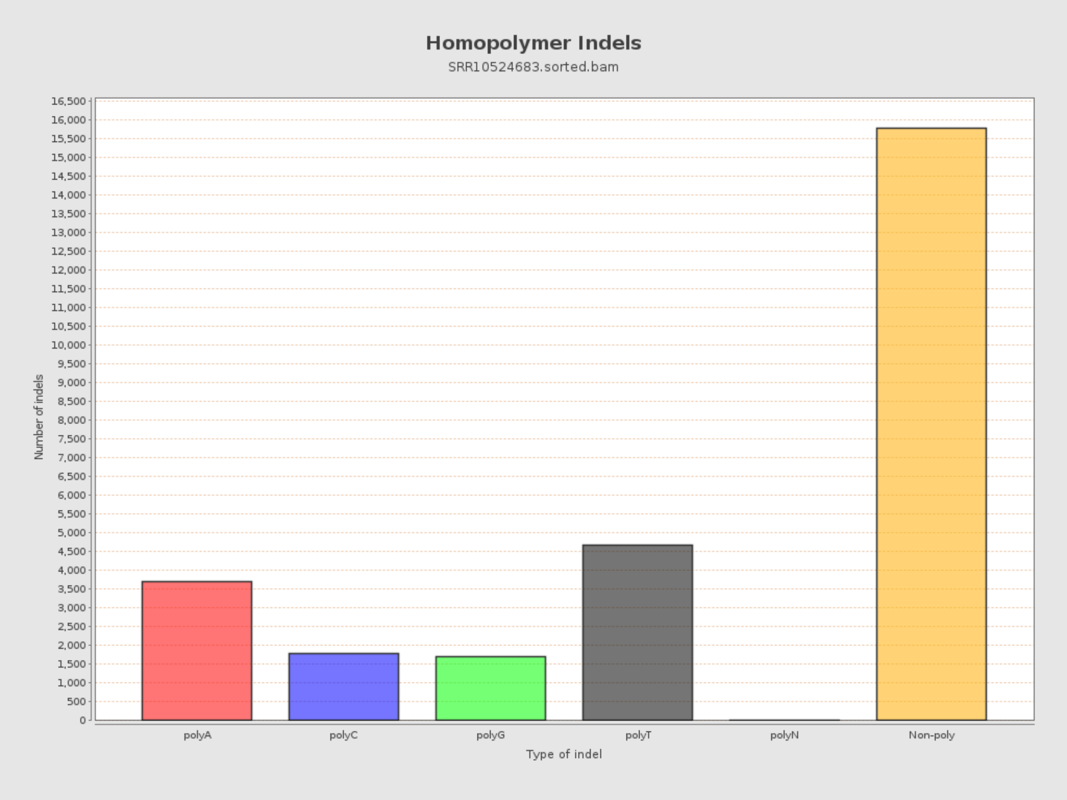
# 9. Results : Mapped Reads GC-content Distribution



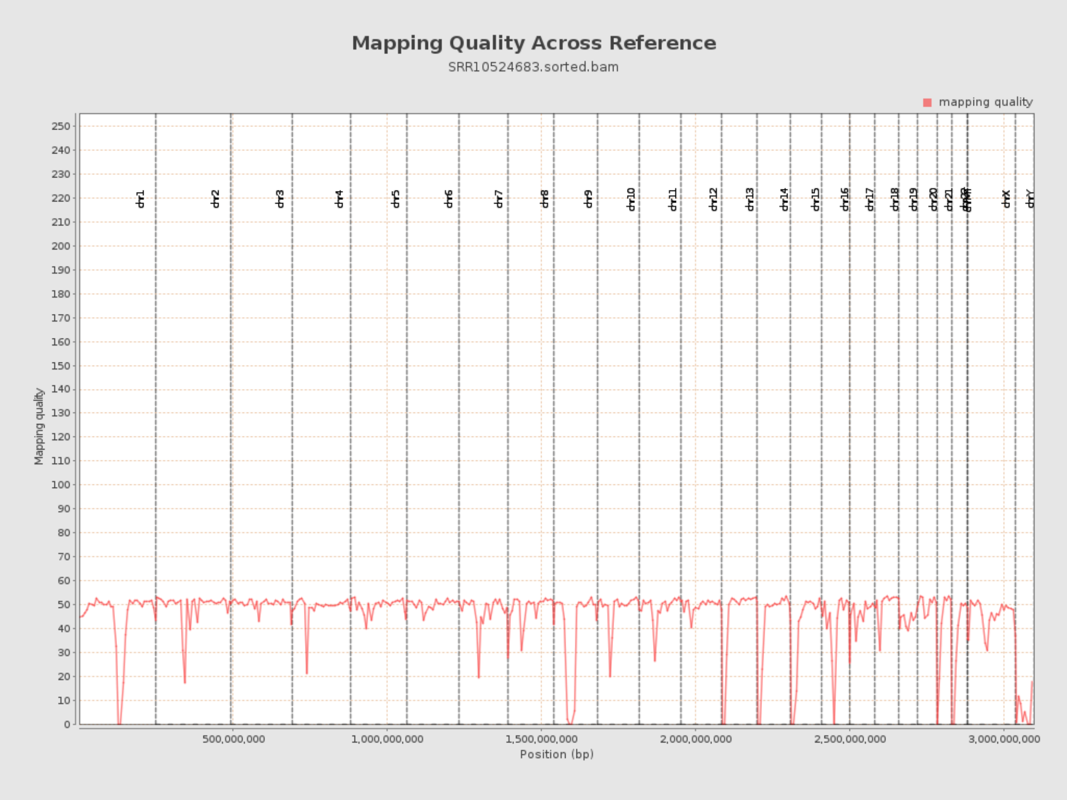
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram